

# RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.

Application Serial Number: 10/049,358A  
Source: 1Fw/b  
Date Processed by STIC: 10/16/06

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IFW16

## RAW SEQUENCE LISTING

DATE: 10/16/2006

PATENT APPLICATION: US/10/049,358A

TIME: 11:01:14

Input Set : A:\PB9944.ST25.txt

Output Set: N:\CRF4\10162006\J049358A.raw

3 <110> APPLICANT: DAVIS, Maria  
 4 NELSON, John  
 5 KUMAR, Shiv  
 6 FINN, Patrick  
 7 NAMPALLI, Satyam  
 8 FLICK, Parke  
 10 <120> TITLE OF INVENTION: TAQ DNA POLYMERASES HAVING AN AMINO ACID SUBSTITUTION AT  
 E681 AND  
 11 HOMOLOGS THEREOF EXHIBITING IMPROVED SALT TOLERANCE  
 13 <130> FILE REFERENCE: PB9944  
 15 <140> CURRENT APPLICATION NUMBER: US 10/049,358A  
 16 <141> CURRENT FILING DATE: 2002-05-17  
 18 <150> PRIOR APPLICATION NUMBER: PCT/US00/22150  
 19 <151> PRIOR FILING DATE: 2000-08-10  
 21 <150> PRIOR APPLICATION NUMBER: US 60/154,739  
 22 <151> PRIOR FILING DATE: 1999-09-17  
 24 <150> PRIOR APPLICATION NUMBER: US 60/150,167  
 25 <151> PRIOR FILING DATE: 1999-08-21  
 27 <160> NUMBER OF SEQ ID NOS: 5  
 29 <170> SOFTWARE: PatentIn version 3.3  
 31 <210> SEQ ID NO: 1  
 32 <211> LENGTH: 832  
 33 <212> TYPE: PRT  
 34 <213> ORGANISM: Thermus aquaticus  
 36 <400> SEQUENCE: 1  
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 42 Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys Gly  
 43 20 25 30  
 46 Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala  
 47 35 40 45  
 50 Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile Val  
 51 50 55 60  
 54 Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly Gly  
 55 65 70 75 80  
 58 Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu  
 59 85 90 95  
 62 Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu Glu  
 63 100 105 110  
 66 Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys Lys  
 67 115 120 125  
 70 Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys Asp  
 71 130 135 140  
 74 Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu Gly

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75 145          150          155          160
78 Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro
79          165          170          175
82 Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp Asn
83          180          185          190
86 Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu Leu
87          195          200          205
90 Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg Leu
91          210          215          220
94 Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu Lys
95 225          230          235          240
98 Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu Val
99          245          250          255
102 Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala Phe
103          260          265          270
106 Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu
107          275          280          285
110 Glu Ser Pro Lys Ala Leu Glu Ala Pro Trp Pro Pro Pro Glu Gly
111          290          295          300
114 Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala Asp
115 305          310          315          320
118 Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala Pro
119          325          330          335
122 Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu Leu
123          340          345          350
126 Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu Pro
127          355          360          365
130 Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn
131          370          375          380
134 Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu
135 385          390          395          400
138 Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn Leu
139          405          410          415
142 Trp Gly Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg Glu
143          420          425          430
146 Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr Gly
147          435          440          445
150 Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val Ala
151          450          455          460
154 Glu Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly His
155 465          470          475          480
158 Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp
159          485          490          495
162 Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys Arg
163          500          505          510
166 Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile
167          515          520          525
170 Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser Thr
171          530          535          540

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174 Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg Leu
175 545                    550                    555                    560
178 His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser
179                    565                    570                    575
182 Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln
183                    580                    585                    590
186 Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val Ala
187                    595                    600                    605
190 Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly
191                    610                    615                    620
194 Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His Thr
195 625                    630                    635                    640
198 Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp Pro
199                    645                    650                    655
202 Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly
203                    660                    665                    670
206 Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu
207                    675                    680                    685
210 Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg
211                    690                    695                    700
214 Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr Val
215 705                    710                    715                    720
218 Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala Arg
219                    725                    730                    735
222 Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro
223                    740                    745                    750
226 Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu
227                    755                    760                    765
230 Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val His
231                    770                    775                    780
234 Asp Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val Ala
235 785                    790                    795                    800
238 Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val Pro
239                    805                    810                    815
242 Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys Glu
243                    820                    825                    830
246 <210> SEQ ID NO: 2
247 <211> LENGTH: 561
248 <212> TYPE: PRT
249 <213> ORGANISM: Thermus aquaticus
251 <400> SEQUENCE: 2
253 Met Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu
254 1                    5                    10                    15
257 Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
258                    20                    25                    30
261 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala
262                    35                    40                    45
265 Asp Leu Leu Ala Leu Ala Ala Arg Gly Gly Arg Val His Arg Ala
266                    50                    55                    60

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269 Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu
270 65          70          75          80
273 Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu
274          85          90          95
277 Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser
278          100         105         110
281 Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr
282          115         120         125
285 Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn
286          130         135         140
289 Leu Trp Gly Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg
290 145          150         155         160
293 Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr
294          165         170         175
297 Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val
298          180         185         190
301 Ala Glu Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly
302          195         200         205
305 His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe
306          210         215         220
309 Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys
310 225          230         235         240
313 Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro
314          245         250         255
317 Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser
318          260         265         270
321 Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg
322          275         280         285
325 Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser
326          290         295         300
329 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly
330 305          310         315         320
333 Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Gly Trp Leu Leu Val
334          325         330         335
337 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser
338          340         345         350
341 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His
342          355         360         365
345 Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp
346          370         375         380
349 Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Tyr Gly Val Leu Tyr
350 385          390         395         400
353 Gly Met Ser Ala His Arg Leu Ser Gln Arg Leu Ala Ile Pro Tyr Glu
354          405         410         415
357 Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val
358          420         425         430
361 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr
362          435         440         445
365 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala

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366      450      455      460
369 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
370 465      470      475      480
373 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
374      485      490      495
377 Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val
378      500      505      510
381 His Asp Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val
382      515      520      525
385 Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val
386      530      535      540
389 Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys
390 545      550      555      560
393 Glu
397 <210> SEQ ID NO: 3
398 <211> LENGTH: 832
399 <212> TYPE: PRT
400 <213> ORGANISM: Thermus aquaticus
402 <400> SEQUENCE: 3
404 Met Arg Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu
405 1      5      10      15
408 Val Ala Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys Gly
409      20      25      30
412 Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala
413      35      40      45
416 Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile Val
417      50      55      60
420 Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly Gly
421 65      70      75      80
424 Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu
425      85      90      95
428 Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu Glu
429      100      105      110
432 Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys Lys
433      115      120      125
436 Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys Asp
437      130      135      140
440 Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu Gly
441 145      150      155      160
444 Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro
445      165      170      175
448 Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp Asn
449      180      185      190
452 Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu Leu
453      195      200      205
456 Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg Leu
457      210      215      220
460 Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu Lys
461 225      230      235      240

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VERIFICATION SUMMARY

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